

GaMYB1_alignment_and_sequence.txt

Exhibit 2

gi|7438345|pir||T09879 myb-related protein A - upland cotton
 gi|437327|gb|AAA33067.1| MYB1 [Gossypium hirsutum]
 gi|23476277|gb|AAN28269.1| myb-like transcription factor 1 [Gossypium hirsutum]

Length = 294
 Score = 602 bits (1553), Expect = e-171
 Identities = 288/294 (97%), Positives = 291/294 (98%)
 Frame = +3

Query: 144 MGRSPCCEKAHTNKGAWTKEEDQRLINIRVHGEWCWRS LPKAAGLLRCGKSCRLRWINY 323
 MGRSPCCEKAHTNKGAWTKEEDQRLINIRVHGEWCWRS LPKAAGLLRCGKSCRLRWINY
 Sbjct: 1 MGRSPCCEKAHTNKGAWTKEEDQRLINIRVHGEWCWRS LPKAAGLLRCGKSCRLRWINY 60
 Query: 324 LRPDLKRGNFTEEEDELI IKLHSL LGNKWSLIAGRLPGR TDNEIKNYWNTHIKRKLISRG 503
 LRPDLKRGNFTEEEDELI IKLHSL LGNKWSLIAGRLPGR TDNEIKNYWNTHIKRKLISRG
 Sbjct: 61 LRPDLKRGNFTEEEDELI IKLHSL LGNKWSLIAGRLPGR TDNEIKNYWNTHIKRKLISRG 120
 Query: 504 IDPQTHRPLNQTAITNTVTGPT ELDFRNSPTSVSKSSSIKNPSLDFNYNEFHKSHTDSL 683
 IDPQTHRPLNQTA TNTVT PTELDFRNSPTSVSKSSSIKNPSLDFNYNEF FKS+TDSL
 Sbjct: 121 IDPQTHRPLNQTAITNTVTAPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFQFKSNTDSL 180
 Query: 684 EEPNCTASTGMTTDEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK 863
 EEPNCTAS+GMTTDEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRV S+ANSAESK
 Sbjct: 181 EEPNCTASSGMTTDEEQEQLHKKQYGPSNGQDINLELSIGIVSADSSRVSNANSAESK 240
 Query: 864 PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFY SYCRPLDS 1025
 PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFY SYCRPLDS
 Sbjct: 241 PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFY SYCRPLDS 294

>Contig20 GaMYB1
 GGCACGAGACAGTTTCTTTTTTGCTCATTTCCATCATCCCCATGTCCC
 CTCTCCATGTTTTCTAAATCTCTCCATATACCTATAACACCGTTATTCT
 TTCTCTATTCTACCTGATTTGATTTGATTTGATTTGTAAGTATGATGGGAC
 GATCACCTTGTGTGAAAAGGCTCATACCAACAAAGGTGCCTGGACCAAA
 GAGGAAGATCAACGCCTCATCAACTACATCCGTGTCCATGGTGAAGGCTG
 CTGGCGTTCCTCCCAAGCTGCTGGGCTGCTTAGATGTGGTAAGAGTT
 GCAGATTAAGATGGATAAACTACTTGAGGCCTGATCTTAAGAGAGGAAAT
 TTCCTGAAGAAGAAGATGAGCTTATCATCAAGCTTCACAGTTTACTTGG
 AAACAAATGGTCATTGATTGCTGGAAGATTACCAGGAAGGACAGATAATG
 AGATAAAGAAGTACTGGAACACACACATCAAAAGAAAGCTTATAAGCAGA
 GGAATTGATCCACAACTCATCGTCCTCTCAATCAAACGGCCATTACCAA
 CACAGTCACAGGCCCCACCGAATTGGATTTAGAACTCGCCACATCCG
 TTTCAAATCCAGTTCCATCAAAAACCGCTCTCTGGATTTCAATTACAAT
 GAATTTCAATTTCAAGTCCCACACAGATTCCTTGAAGAACCCAACTGTAC
 AGCCAGCACTGGCATGACTACAGATGAAGAACAACAAGACAGCTGCACA
 AGAAGCAGCAATACGGTCCGAGCAATGGGCAAGACATAAATTTGGAGCTG
 TCGATTGGGATTGTTTCAGCTGACTCATCTCGGGTATCAAGTGCCAACTC
 GGCCGAGTCGAAACCAAGGTAGATAACAACAATTTCCAGTTTCTTGAAC
 AAGCTATGGTGGCTAAGGCGGTATGTTTGTGTTGGCAATTAGGTTTTGGA
 ACAAGTGAAATTTGTAGGAAGTGTCAAAATTCAAATTCAAATGGCTTCTA
 TAGTTATTGTAGACCTTGGATTATAGGGTCATCTTTTCTTCTTCTTCTT
 TCTGTTTTTAGGAGATAAATTAATTCTTAATTATTATCTTTTGCCTGCC
 CACTGTAATCAAAGCAAAATTATAAAACAAAGACTCTTTTGGATTTGTTT
 AATTTATAGGTTCAAAAAAAAAAAAAAAAAAAAA

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>Contig20_Frame+3 GaMYB1

HETVSLFCSFPSSPCPLSMFF*ISPYTYNTVILSLFYLI*FDLIL*LMGRSPCCEKAHTN
KGAWTKEEDQRLINYIRVHGEWCWRSPLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE
EDELI IKLHSL LGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRGIDPQTHRPLNQTA
ITNTVTGPTELD FRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSLEEPNCTASTGMTT
DEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESKPKVDNNNFQFLEQ
AMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS*GHLFLLSFCF*EIN*FLI
IIFLPAHCNQSKI IKQRLFLICSIYRFKKKKKK

>GaMYB1 - putative from GhMYB1 alignment

MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEWCWRSPLPKAAGLLRCGKSCRLRWINY
LRPDLKRGNFTEEEDELI IKLHSL LGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG
IDPQTHRPLNQTAITNTVTGPTELD FRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSL
EEP NCTASTGMTTDEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK
PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS